Quinoa genetic diversity and structure and how it impacts plant breeding

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The countries of Peru and Bolivia produce much of the quinoa the world consumes, but countries outside of South America are beginning to experiment with and grow quinoa. Plant breeders interested in quinoa improvement and adaptation to the new growing regions must develop core germplasm collections for use in pre-breeding experiments and breeding schemes, and will need to evaluate the genetic diversity of existing international *ex situ* germplasm collections. Plant breeders know well the need for genetic variation, and the greater the diversity represented in a germplasm collection, the better. It is well known that quinoa suffered a major bottleneck when the crop nearly went extinct following the Spanish conquest. Since the 1980's, quinoa diversity has been characterized both morphologically and molecularly. With each more informative molecular technique, Wilson's (1988) conclusions are reaffirmed:

- The center of quinoa diversity is in the southern Andean highlands
- Quinoa varieties are genetically grouped into two main groups: lowland and highland

Recent molecular studies of quinoa genetic diversity have revealed that germplasm collections lack accessions from many of the smaller, but significant, growing regions of Argentina, Colombia, Ecuador and the Bolivian Yungas region (Christensen et al., 2007). Such underrepresented areas could host quinoa with traits useful in other (and new) growing regions. High genetic heterogeneity within accessions has been found, and this could due to outcrossing during seed maintenance and/or the accession being a heterogeneous landrace that has low phenotypic diversity. As studies focus on smaller quinoa growing regions, researchers are discovering that these regions host great genetic diversity despite being far away from the center of origin. Costa Tártara et al. (2012) characterized northwest Argentinean (NWA) quinoa into four distinct groups that match the different environments of origin, cultural practices, and societal isolation. Fuentes et al. (2012) took a refreshingly new look at quinoa genetic structure by matching it with natural geographical edaphic climatic constraints and the social linguistic context of ancient people inhabiting the Andes region. The researchers uncovered surprisingly greater genetic diversity within Chilean quinoa than what previous studies had estimated (Christensen et al., 2007). This being said, the researchers believe bottlenecking has occurred within lowland guinoa and the conclusion matches farmer isolation in the area. With the increase in molecular studies, the five major quinoa ecotypes established with morphometric data by Tapia et al. (1980) were becoming suspect. Fuentes et al. (2012), however, confirm the ecotypes. Quinoa genetic diversity is at risk. Genetic erosion is possible as farmers decrease field diversity in favor of export markets and as farmers abandon rural areas for urban incentives leaving landraces once long cultivated to go extinct.

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